#7

SEQUENCE LISTING

<110> Darrow, Andrew
Qi, Jenson
Andrade-Grodon, Patricia

<120> Zymogen Activation System

<130> ORT-1552

<140> 10/015,989
<141> 2001-12-10

<150> 09/303,162
<151> 1999-04-30

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<170> PatentIn version 3.2

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gtggacgcgg ccgctcttgc tgcccccttt gatgatgatg acaagatcgt tgggggctat 180

gctctagata gcggccgctt ccctttagtg agggttaatg cttcgagcag acatgataag 240

atacattgat gagtttggac aaaccacaac tagaatgcag tgaaaaaaat gctttatttg 300

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atacattgat gagtttggac aaaccacaac tagaatgcag tgaaaaaaat gctttatttg 240

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ctagataccc ctacgatgtg cccgattacg ccgctagata cccctacgat gtgcccgatt 240

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gtggacgcgg ccgctcttgc tgccccctttt gatgatgatg acaagatcgt tgggggctac 180

aactgtctag acatcaccat caccatcact agcggccgct tccctttagt gagggttaat 240

gcttcgagca gacatgataa gatacattga tgagtttgga caaaccacaa ctagaatgca 300

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agcggccgct tccctttagt gagggttaat gcttcgagca gacatgataa gatacattga 240

tgagtttgga caaaccacaa ctagaatgca gtgaaaaaaa tgctttattt gtgaaatttg 300

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attacgccgc tagacatcac catcaccatc actagcggcc gcttcccttt agtgagggtt 240

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tgtggtggct ctctcgtgtc tgagcagtgg gtgctgtcag ctgctcactg cttccccagc 300

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caactcgagg tgcctctgat cagtcgtgag acgtgtaact gcctgtacaa catcgacgcc 660

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cctcgtgtgg tgccccaaac ccaggagtcc cagcccgaca gcaacctctg tggcagccac 960

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ggttaatgct tcgagcagac atgataagat acattgatga gtttggacaa accacaacta 1080

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ccattataag ctgcaataaa caagttgac 1169

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<211> 1142
<212> DNA
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tttgatgatg atgacaagat cgttgggggc tatgctctag aggccggtca gtggccctgg 180

caggtcagca tcacctatga aggcgtccat gtgtgtggtg gctctctcgt gtctgagcag 240

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aagctggggg cccaccagct agactcctac tccgaggacg ccaaggtcag caccctgaag 360

gacatcatcc cccaccccag ctacctccag gagggctccc agggcgacat tgcactcctc 420

caactcagca gacccatcac cttctcccgc tacatccggc ccatctgcct ccctgcagcc 480

aacgcctcct tccccaacgg cctccactgc actgtcactg gctggggtca tgtggccccc 540

tcagtgagcc tcctgacgcc caagccactg cagcaactcg aggtgcctct gatcagtcgt 600

gagacgtgta actgcctgta caacatcgac gccaagcctg aggagccgca ctttgtccaa 660

gaggacatgg tgtgtgctgg ctatgtggag gggggcaagg acgcctgcca gggtgactct 720

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tcccagcccg acagcaacct ctgtggcagc cacctggcct tcagctctag acatcaccat 960

caccatcact agcggccgct tccctttagt gagggttaat gcttcgagca gacatgataa 1020

gatacattga tgagtttgga caaaccacaa ctagaatgca gtgaaaaaaa tgctttattt 1080

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aactgtctag aaccccattc gcagccttgg caggcggcct tgttccaggg ccagcaacta 240

ctctgtggcg gtgtccttgt aggtggcaac tgggtcctta cagctgccca ctgtaaaaaa 300

ccgaaataca cagtacgcct gggagaccac agcctacaga ataaagatgg cccagagcaa 360

gaaatacctg tggttcagtc catcccacac ccctgctaca acagcagcga tgtggaggac 420

cacaaccatg atctgatgct tcttcaactg cgtgaccagg catccctggg gtccaaagtg 480

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ggcagcaagg gctctagaca tcaccatcac catcactagc ggccgcttcc ctttagtgag 900

ggttaatgct tcgagcagac atgataagat acattgatga gtttggacaa accacaacta 960

gaatgcagtg aaaaaaatgc tttatttgtg aaatttgtga tgctattgct ttatttgtaa 1020

ccattataag ctgcaataaa caagttgac 1049

<210> 10
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<223> Fusion Gene With Homo Sapien Serine Protease Catalytic Domain

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gtggacgcgg ccgctcttgc tgccccctttt gatgatgatg acaagatcgt tgggggctac 180

aactgtctag aaaagcactc ccagccctgg caggcagccc tgttcgagaa gacgcggcta 240

ctctgtgggg cgacgctcat cgcccccaga tggctcctga cagcagccca ctgcctcaag 300

ccccgctaca tagttcacct ggggcagcac aacctccaga aggaggaggg ctgtgagcag 360

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<400> 11

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Val Val Ser Asn Leu Leu Leu Cys Gln Gly Val Val Ser Asp Tyr Lys
20 25 30

Asp Asp Asp Asp Val Asp Ala Ala Ala Leu Ala Ala Pro Phe Asp Asp
35 40 45

Asp Asp Lys Ile Val Gly Gly Tyr Ala Leu Glu Ala Gly Gln Trp Pro
50 55 60

Trp Gln Val Ser Ile Thr Tyr Glu Gly Val His Val Cys Gly Gly Ser
65 70 75 80

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Leu Val Ser Glu Gln Trp Val Leu Ser Ala Ala His Cys Phe Pro Ser
                85                  90                  95

Glu His His Lys Glu Ala Tyr Glu Val Lys Leu Gly Ala His Gln Leu
            100                 105                 110

Asp Ser Tyr Ser Glu Asp Ala Lys Val Ser Thr Leu Lys Asp Ile Ile
        115                 120                 125

Pro His Pro Ser Tyr Leu Gln Glu Gly Ser Gln Gly Asp Ile Ala Leu
    130                 135                 140

Leu Gln Leu Ser Arg Pro Ile Thr Phe Ser Arg Tyr Ile Arg Pro Ile
145                 150                 155                 160

Cys Leu Pro Ala Ala Asn Ala Ser Phe Pro Asn Gly Leu His Cys Thr
                165                 170                 175

Val Thr Gly Trp Gly His Val Ala Pro Ser Val Ser Leu Leu Thr Pro
            180                 185                 190

Lys Pro Leu Gln Gln Leu Glu Val Pro Leu Ile Ser Arg Glu Thr Cys
        195                 200                 205

Asn Cys Leu Tyr Asn Ile Asp Ala Lys Pro Glu Glu Pro His Phe Val
    210                 215                 220

Gln Glu Asp Met Val Cys Ala Gly Tyr Val Glu Gly Gly Lys Asp Ala
225                 230                 235                 240

Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Cys Pro Val Glu Gly Leu
                245                 250                 255

Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Asp Ala Cys Gly Ala Arg
            260                 265                 270

Asn Arg Pro Gly Val Tyr Thr Leu Ala Ser Ser Tyr Ala Ser Trp Ile
        275                 280                 285

Gln Ser Lys Val Thr Glu Leu Gln Pro Arg Val Val Pro Gln Thr Gln
    290                 295                 300

Glu Ser Gln Pro Asp Ser Asn Leu Cys Gly Ser His Leu Ala Phe Ser
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Ser Arg His His His His His His
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<210> 12
<211> 319
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Gene With Homo Sapien Serine Protease Catalytic Domain

<400> 12

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Phe Gly Cys Gly Val Pro Asp Tyr Lys Asp Asp Asp Asp Ala Ala Ala
20 25 30

Leu Ala Ala Pro Phe Asp Asp Asp Asp Lys Ile Val Gly Gly Tyr Ala
35 40 45

Leu Glu Ala Gly Gln Trp Pro Trp Gln Val Ser Ile Thr Tyr Glu Gly
50 55 60

Val His Val Cys Gly Gly Ser Leu Val Ser Glu Gln Trp Val Leu Ser
65 70 75 80

Ala Ala His Cys Phe Pro Ser Glu His His Lys Glu Ala Tyr Glu Val
85 90 95

Lys Leu Gly Ala His Gln Leu Asp Ser Tyr Ser Glu Asp Ala Lys Val
100 105 110

Ser Thr Leu Lys Asp Ile Ile Pro His Pro Ser Tyr Leu Gln Glu Gly
115 120 125

Ser Gln Gly Asp Ile Ala Leu Leu Gln Leu Ser Arg Pro Ile Thr Phe
130 135 140

Ser Arg Tyr Ile Arg Pro Ile Cys Leu Pro Ala Ala Asn Ala Ser Phe
145 150 155 160

Pro Asn Gly Leu His Cys Thr Val Thr Gly Trp Gly His Val Ala Pro
165 170 175

Ser Val Ser Leu Leu Thr Pro Lys Pro Leu Gln Gln Leu Glu Val Pro
180 185 190

Leu Ile Ser Arg Glu Thr Cys Asn Cys Leu Tyr Asn Ile Asp Ala Lys
195 200 205

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Pro Glu Glu Pro His Phe Val Gln Glu Asp Met Val Cys Ala Gly Tyr
    210                 215                 220

Val Glu Gly Gly Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu
225                 230                 235                 240

Ser Cys Pro Val Glu Gly Leu Trp Tyr Leu Thr Gly Ile Val Ser Trp
                245                 250                 255

Gly Asp Ala Cys Gly Ala Arg Asn Arg Pro Gly Val Tyr Thr Leu Ala
            260                 265                 270

Ser Ser Tyr Ala Ser Trp Ile Gln Ser Lys Val Thr Glu Leu Gln Pro
        275                 280                 285

Arg Val Val Pro Gln Thr Gln Glu Ser Gln Pro Asp Ser Asn Leu Cys
    290                 295                 300

Gly Ser His Leu Ala Phe Ser Ser Arg His His His His His His
305                 310                 315
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<210> 13
<211> 288
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Gene With Homo Sapien Serine Protease Catalytic Domain

<400> 13

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Val Val Ser Asn Leu Leu Leu Cys Gln Gly Val Val Ser Asp Tyr Lys
            20                  25                  30

Asp Asp Asp Asp Val Asp Ala Ala Ala Leu Ala Ala Pro Phe Asp Asp
        35                  40                  45

Asp Asp Lys Ile Val Gly Gly Tyr Asn Cys Leu Glu Pro His Ser Gln
    50                  55                  60

Pro Trp Gln Ala Ala Leu Phe Gln Gly Gln Gln Leu Leu Cys Gly Gly
65                  70                  75                  80

Val Leu Val Gly Gly Asn Trp Val Leu Thr Ala Ala His Cys Lys Lys
                85                  90                  95

Pro Lys Tyr Thr Val Arg Leu Gly Asp His Ser Leu Gln Asn Lys Asp
            100                 105                 110
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Gly Pro Glu Gln Glu Ile Pro Val Val Gln Ser Ile Pro His Pro Cys
        115                 120                 125

Tyr Asn Ser Ser Asp Val Glu Asp His Asn His Asp Leu Met Leu Leu
    130                 135                 140

Gln Leu Arg Asp Gln Ala Ser Leu Gly Ser Lys Val Lys Pro Ile Ser
145                 150                 155                 160

Leu Ala Asp His Cys Thr Gln Pro Gly Gln Lys Cys Thr Val Ser Gly
                165                 170                 175

Trp Gly Thr Val Thr Ser Pro Arg Glu Asn Phe Pro Asp Thr Leu Asn
            180                 185                 190

Cys Ala Glu Val Lys Ile Phe Pro Gln Lys Lys Cys Glu Asp Ala Tyr
        195                 200                 205

Pro Gly Gln Ile Thr Asp Gly Met Val Cys Ala Gly Ser Ser Lys Gly
    210                 215                 220

Ala Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asp Gly
225                 230                 235                 240

Ala Leu Gln Gly Ile Thr Ser Trp Gly Ser Asp Pro Cys Gly Arg Ser
                245                 250                 255

Asp Lys Pro Gly Val Tyr Thr Asn Ile Cys Arg Tyr Leu Asp Trp Ile
            260                 265                 270

Lys Lys Ile Ile Gly Ser Lys Gly Ser Arg His His His His His His
        275                 280                 285
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<210> 14
<211> 289
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Gene With Homo Sapien Serine Protease Catalytic Domain

<400> 14

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            20                  25                  30
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Asp Asp Asp Asp Val Asp Ala Ala Ala Leu Ala Ala Pro Phe Asp Asp
        35                  40                  45

Asp Asp Lys Ile Val Gly Gly Tyr Asn Cys Leu Glu Lys His Ser Gln
    50                  55                  60

Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly Ala
65                  70                  75                  80

Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu Lys
                85                  90                  95

Pro Arg Tyr Ile Val His Leu Gly Gln His Asn Leu Gln Lys Glu Glu
            100                 105                 110

Gly Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro Gly
        115                 120                 125

Phe Asn Asn Ser Leu Pro Asn Lys Asp His Arg Asn Asp Ile Met Leu
    130                 135                 140

Val Lys Met Ala Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro Leu
145                 150                 155                 160

Thr Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Leu Ile Ser
                165                 170                 175

Gly Trp Gly Ser Thr Ser Ser Pro Gln Leu Arg Leu Pro His Thr Leu
            180                 185                 190

Arg Cys Ala Asn Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn Ala
        195                 200                 205

Tyr Pro Gly Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln Glu
    210                 215                 220

Gly Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
225                 230                 235                 240

Asn Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala
                245                 250                 255

Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val Asp
            260                 265                 270

Trp Ile Gln Glu Thr Met Lys Asn Asn Ser Arg His His His His His
        275                 280                 285
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His

<210> 15
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 15
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<210> 16
<211> 9
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<213> Artificial Sequence

<220>
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<400> 16
ggccgctat 9

<210> 17
<211> 36
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<220>
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<400> 17
ctagataccc ctacgatgtg cccgattacg cctagc 36

<210> 18
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<212> DNA
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<210> 19
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<400> 21
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<400> 22
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<210> 23
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<212> DNA
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<400> 23
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<210> 24
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<220>
<223> Oligonucleotide

<400> 24
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<210> 25
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<220>
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<400> 25
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<210> 26
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<212> DNA
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<220>
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<400> 26
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<220>
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<400> 27
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<210> 28
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<400> 28
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<210> 29
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<220>
<223> Oligonucleotide

<400> 29
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<210> 30
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 30
ggcacaagag tagatttgac accaccagca 30

<210> 31
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 31
gcaggagcag gcgggaccct ttctgcgacg 30

<210> 32
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 32
aacctttgct gtccatggtg gtgaattca 29

<210> 33
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 33
aattcaccat gaatccactc ctgatcctta cctttgtggc 40

<210> 34
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 34
ggccgccaca aaggtaagga tcaggagtgg attcatggtg 40

<210> 35
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 35
aattcaccac catggctttc ctctggctcc tctcctgctg ggccctcctg ggtac 55

<210> 36
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 36
ccaggagggc ccagcaggag aggagccaga ggaaagccat ggtggtg 47

<210> 37
<211> 45
<212> DNA
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<220>
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<400> 37
caccttcggc tgcggggtcc ccgactacaa ggacgacgac gacgc 45

<210> 38
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 38
ggccgcgtcg tcgtcgtcct tgtagtcggg gaccccgcag ccgaaggtgg tac 53

<210> 39
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
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<400> 39
gtggcggccg ctcttgctgc ccccttga 29

<210> 40
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 40
ttctctagac agttgtagcc cccaacga 28

<210> 41
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 41
ggccgctctt gctgcccccc ttgatgatga tgacaagatc gttgggggct atgct 55

<210> 42
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 42
ctagagcata gcccccaacg atcttgtcat catcatcaaa gggggcagca agagc 55

<210> 43
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 43
ggccgctctt gctgcccccc ttgatgatga tgacaagatc gttgggggct attgt 55

<210> 44
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 44
ctagacaata gcccccaacg atcttgtcat catcatcaaa gggggcagca agagc 55

<210> 45
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 45
ggccgctctt gctgcccccc ttatcgaggg gcgcattgtg gagggctcgg at 52

<210> 46
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 46
ctagatccga gccctccaca atgcgcccct cgataaaggg ggcagcaaga gc 52

<210> 47
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 47
agcagtctag aggccggtca gtggccctgg ca 32

<210> 48
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 48
gctggtctag agctgaaggc caggtggc 28

<210> 49
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 49
ggtatctaga gcccttgctg cctatgatc 29

<210> 50
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 50
actgtctaga accccattcg cagccttggc 30

<210> 51
<211> 32
<212> DNA
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<220>
<223> Oligonucleotide

<400> 51
tcgatctaga aaagcactcc cagccctggc ag 32

<210> 52
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 52
gtcctctaga attgttcttc atcgtctcct gg 32

<210> 53
<211> 306
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Gene Of Human Protease F In CFEK2 Zymogen Vector

<400> 53

Met Ala Phe Leu Trp Leu Leu Ser Cys Trp Ala Leu Leu Gly Thr Thr
1 5 10 15

Phe Gly Cys Gly Val Pro Asp Tyr Lys Asp Asp Asp Asp Ala Ala Ala
20 25 30

Leu Ala Ala Pro Phe Asp Asp Asp Asp Lys Ile Val Gly Gly Tyr Ala
35 40 45

Leu Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg Leu Trp Asp
50 55 60

Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg Trp Ala Leu Thr
65 70 75 80

Ala Ala His Cys Phe Glu Thr Tyr Ser Asp Leu Ser Asp Pro Ser Gly
85 90 95

Trp Met Val Gln Phe Gly Gln Leu Thr Ser Met Pro Ser Phe Trp Ser
100 105 110

Leu Gln Ala Tyr Tyr Asn Arg Tyr Phe Val Ser Asn Ile Tyr Leu Ser
115 120 125

Pro Arg Tyr Leu Gly Asn Ser Pro Tyr Asp Ile Ala Leu Val Lys Leu
130 135 140

Ser Ala Pro Val Thr Tyr Thr Lys His Ile Gln Pro Ile Cys Leu Gln
145 150 155 160

Ala Ser Thr Phe Glu Phe Glu Asn Arg Thr Asp Cys Trp Val Thr Gly
165 170 175

```
Trp Gly Tyr Ile Lys Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu
            180                 185                 190

Gln Glu Val Gln Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu
        195                 200                 205

Phe Leu Lys Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys
    210                 215                 220

Ala Gly Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly
225                 230                 235                 240

Gly Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val
                245                 250                 255

Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val Tyr
            260                 265                 270

Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met Ala Gln
        275                 280                 285

Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Ser Arg His His His His
    290                 295                 300

His His
305
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<210> 54
<211> 284
<212> PRT
<213> Artificial Sequence

<220>
<223> Human MH2 Protease In PFEK Zymogen Vector

<400> 54

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Met Asp Ser Lys Gly Ser Ser Gln Lys Ser Arg Leu Leu Leu Leu Leu
1               5                   10                  15

Val Val Ser Asn Leu Leu Leu Cys Gln Gly Val Val Ser Asp Tyr Lys
            20                  25                  30

Asp Asp Asp Asp Val Asp Ala Ala Ala Leu Ala Ala Pro Phe Asp Asp
        35                  40                  45

Asp Asp Lys Ile Val Gly Gly Tyr Asn Cys Leu Glu Pro His Ser Gln
    50                  55                  60
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Pro Trp Gln Ala Ala Leu Val Met Glu Asn Glu Leu Phe Cys Ser Gly
65                  70                  75                  80

Val Leu Val His Pro Gln Trp Val Leu Ser Ala Ala His Cys Phe Gln
                85                  90                  95

Asn Ser Tyr Thr Ile Gly Leu Gly Leu His Ser Leu Glu Ala Asp Gln
            100                 105                 110

Glu Pro Gly Ser Gln Met Val Glu Ala Ser Leu Ser Val Arg His Pro
        115                 120                 125

Glu Tyr Asn Arg Pro Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu
    130                 135                 140

Asp Glu Ser Val Ser Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala
145                 150                 155                 160

Ser Gln Cys Pro Thr Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly
                165                 170                 175

Leu Leu Ala Asn Gly Arg Met Pro Thr Val Leu Gln Cys Val Asn Val
            180                 185                 190

Ser Val Val Ser Glu Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr
        195                 200                 205

His Pro Ser Met Phe Cys Ala Gly Gly Gly His Asp Gln Lys Asp Ser
    210                 215                 220

Cys Asn Gly Asp Ser Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln
225                 230                 235                 240

Gly Leu Val Ser Phe Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro
                245                 250                 255

Gly Val Tyr Thr Asn Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr
            260                 265                 270

Val Gln Ala Ser Ser Arg His His His His His His
        275                 280
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<210> 55
<211> 30
<212> DNA
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<220>
<223> PCR Primer

<400> 55
aggatctaga gccgcactcg cagccctggc 30

<210> 56
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 56
cccatctaga actggcctgg acggttttct 30

<210> 57
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 57
aggatctaga actcgggcgt tggccgtggc ag 32

<210> 58
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 58
agagtctaga ccaggagggg tctggctggg 30

<210> 59
<211> 1103
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic Acid Sequence Of Human Protease F In CFEK2 Zymogen Vector

<400> 59
gaattcacca ccatggcttt cctctggctc ctctcctgct gggccctcct gggtaccacc 60

ttcggctgcg gggtccccga ctacaaggac gacgacgacg cggccgctct tgctgccccc 120

tttgatgatg atgacaagat cgttgggggc tatgctctag aactcgggcg ttggccgtgg 180

caggggagcc tgcgcctgtg ggattcccac gtatgcggag tgagcctgct cagccaccgc 240

tgggcactca cggcggcgca ctgctttgaa acctatagtg accttagtga tccctccggg 300

tggatggtcc agtttggcca gctgacttcc atgccatcct tctggagcct gcaggcctac 360

tacaaccgtt acttcgtatc gaatatctat ctgagccctc gctacctggg gaattcaccc 420

tatgacattg ccttggtgaa gctgtctgca cctgtcacct acactaaaca catccagccc 480

atctgtctcc aggcctccac atttgagttt gagaaccgga cagactgctg ggtgactggc 540

tgggggtaca tcaaagagga tgaggcactg ccatctcccc acaccctcca ggaagttcag 600

gtcgccatca taaacaactc tatgtgcaac cacctcttcc tcaagtacag tttccgcaag 660

gacatctttg gagacatggt ttgtgctggc aatgcccaag gcgggaagga tgcctgcttc 720

ggtgactcag gtggaccctt ggcctgtaac aagaatggac tgtggtatca gattggagtc 780

gtgagctggg gagtgggctg tggtcggccc aatcggcccg gtgtctacac caatatcagc 840

caccactttg agtggatcca gaagctgatg gcccagagtg gcatgtccca gccagacccc 900

tcctggtcta gacatcacca tcaccatcac tagcggccgc ttccctttag tgagggttaa 960

tgcttcgagc agacatgata agatacattg atgagtttgg acaaaccaca actagaatgc 1020

agtgaaaaaa atgctttatt tgtgaaattt gtgatgctat tgctttattt gtaaccatta 1080

taagctgcaa taaacaagtt gac 1103

<210> 60
<211> 1037
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic Acid Sequence Of Human MH2 Protease In PFEK Zymogen Vector

<400> 60
gaattcacca ccatggacag caaaggttcg tcgcagaaat cccgcctgct cctgctgctg 60

gtggtgtcaa atctactctt gtgccagggt gtggtctccg actacaagga cgacgacgac 120

gtggacgcgg ccgctcttgc tgccccctttt gatgatgatg acaagatcgt tgggggctac 180

aactgtctag agccgcactc gcagccctgg caggcggcac tggtcatgga aaacgaattg 240

ttctgctcgg gcgtcctggt gcatccgcag tgggtgctgt cagccgcaca ctgtttccag 300

aactcctaca ccatcgggct gggcctgcac agtcttgagg ccgaccaaga gccagggagc 360

cagatggtgg aggccagcct ctccgtacgg cacccagagt acaacagacc cttgctcgct 420

aacgacctca tgctcatcaa gttggacgaa tccgtgtccg agtctgacac catccggagc 480

atcagcattg cttcgcagtg ccctaccgcg gggaactctt gcctcgtttc tggctggggt 540

ctgctggcga acggcagaat gcctaccgtg ctgcagtgcg tgaacgtgtc ggtggtgtct 600

gaggaggtct gcagtaagct ctatgacccg ctgtaccacc ccagcatgtt ctgcgccggc 660

ggagggcacg accagaagga ctcctgcaac ggtgactctg gggggcccct gatctgcaac 720

gggtacttgc agggccttgt gtctttcgga aaagccccgt gtggccaagt tggcgtgcca 780

ggtgtctaca ccaacctctg caaattcact gagtggatag agaaaaccgt ccaggccagt 840

tctagacatc accatcacca tcactagcgg ccgcttccct ttagtgaggg ttaatgcttc 900

gagcagacat gataagatac attgatgagt ttggacaaac cacaactaga atgcagtgaa 960

aaaaatgctt tatttgtgaa atttgtgatg ctattgcttt atttgtaacc attataagct 1020

gcaataaaca agttgac 1037